

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Campbell, Robert K.  
Jameson, Bradford A.  
Chappel, Scott C.

(ii) TITLE OF INVENTION: HYBRID PROTEINS

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 22207

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/011,936  
(B) FILING DATE: 20 February 1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Browdy, Roger L.  
(B) REGISTRATION NUMBER: 25,618  
(C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 278..1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTGG GCACAATGTG TCCTGAGGGG	60
AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCT CAGGTTGGG GCTTCTCAAT	120
CTCACTATCG CCATGTAAGC CCAGTATTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA	180
GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT	240
CCGGCTCCCT CTGTTGCCCT CTGGTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC	295
Ser Arg Thr Ser Leu Leu	

CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala 10 15 20	343
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 25 30 35	391
ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 40 45 50	439
CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 55 60 65 70	487
TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 75 80 85	535
TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 90 95 100	583
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 105 110 115	631
AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly 120 125 130	679
ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 135 140 145 150	727
CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT His Ala Gly Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala Gly 155 160 165	775
GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe 170 175 180	823
TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser 185 190 195	871
AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln 200 205 210	919
AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn 215 220 225 230	967
AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys 235 240 245	1015
CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT TA AG His Cys Ser Thr Cys Tyr Tyr His Lys Ser 250 255	1049

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp  
1 5 10 15

Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile  
20 25 30

His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr  
35 40 45

Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg  
50 55 60

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His  
65 70 75 80

Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile  
85 90 95

Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn  
100 105 110

Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys  
115 120 125

Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln  
130 135 140

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu  
145 150 155 160

Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu  
165 170 175

Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys  
180 185 190

Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys  
195 200 205

Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys  
210 215 220

Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val  
225 230 235 240

Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser  
245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 279..1199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGAGATGG	CTACAGGTAA	GCGCCCTAA	AATCCCTTG	GGCACAAATGT	GTCCTGAGGG	60										
GAGAGGTAGC	GACCTGTAGA	TGGGACGGGG	GCACTAACCC	TGAGGTTTGG	GGCTTCTGAA	120										
TGTGAGTATC	GCCATGTAAG	CCCAGTATT	GGCCAATGTC	AGAAAAGCTCC	TGGTCCCTGG	180										
AGGGATGGAG	AGAGAAAAAC	AAACAGCTCC	TGGAGCAGGG	AGAGTGCTGG	CCTCTTGCTC	240										
TCCGGCTCCC	TCTGTTGCC	TGTGGTTCT	CCCCAGGC	TCC	CGG	ACG	TCC	CTG	293							
			Ser	Arg	Thr	Ser	Leu		260							
CTC	CTG	GCT	TTT	GGC	CTG	CTC	TGC	CTG	CCC	TGG	CTT	CAA	GAG	GGC	AGT	341
Leu	Leu	Ala	Phe	Gly	Leu	Leu	Cys	Leu	Pro	Trp	Leu	Gln	Glu	Gly	Ser	
			265				270					275				
GCC	GAT	AGT	GTG	TGT	CCC	CAA	GGA	AAA	TAT	ATC	CAC	CCT	CAA	AAT	AAT	389
Ala	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	
	280			285			290									
TCG	ATT	TGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	437
Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	
	295				300				305							
TGT	CCA	GGC	CCG	GGG	CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	485
Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	
	310			315			320			325						
TCT	TTC	ACC	GCT	TCA	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	533
Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	
	330				335			340								
AAA	TGC	CGA	AAG	GAA	ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	581
Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	
	345			350			355									
GAC	CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	629
Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	
	360			365			370									
TGG	AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	677
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	
	375			380			385									
GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	725
Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	
	390			395			400			405						
TGC	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	GCT	773
Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ala	
	410			415			420									
GGT	GCT	GGT	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	ACC	CTG	GCT	GTG	GAG	821
Gly	Ala	Gly	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala	Val	Glu	
	425			430			435									
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	ACC	ACC	ATC	TGT	GCC	869
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	Cys	Ala	
	440			445			450									

GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTC CCC GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala 455 460 465	917
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile 470 475 480 485	965
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCT Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala 490 495 500	1013
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp 505 510 515	1061
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe 520 525 530	1109
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA Gln Asp Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro 535 540 545	1157
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA TAA Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln 550 555 560	1202

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp 1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile 20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr 35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg 50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His 65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile 85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn 100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys 115 120 125
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln 130 135 140

Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu
145															160
150															
Cys	Val	Ser	Cys	Ala	Gly	Ala	Gly	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala
															175
165															
Thr	Leu	Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn
															190
180															
Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln
															205
195															
Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val
															220
210															
Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro
															240
225															
230	235														
Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg
															255
245															
250															
Arg	Ser	Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys
															270
260															
Asp	Asp	Pro	Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro
															285
275															
Ser	Leu	Pro	Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile
															300
290															
295															
Leu	Pro	Gln													
305															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 278..1132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGAGATGGC TACAGGTAAG CGCCCCCTAAA ATCCCTTGG GCACAATGTG TCCTGAGGGG	60
AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCCT CAGGTTGGG GCTTTGAAT	120
GTGAGTATGG CCATGTAAGC CCAGTATTTG CCCAATCTCA GAAAGCTCCT GGTCCTGGA	180
GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA CACTCCTGGC CTCTTGCTCT	240
GGGGCTCCGT GTGTTGCCCT GTGGTTCTC CCCACGC TCC CGG ACG TCC CTG CTC	295
Ser Arg Thr Ser Leu Leu	
310	
CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC	343
Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala	
315 320 325	

GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 330 335 340 345	391
ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 350 355 360	439
CCA GGC CCG GGG CAG GAT ACC GAC TGC AGG GAG TGT GAG AGC GGC TCC Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 365 370 375	487
TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 380 385 390	535
TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 395 400 405	583
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CCG CAT TAT TGG Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 410 415 420 425	631
AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC ACC CTC TGC CTC AAT GGG Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Thr Leu Cys Leu Asn Gly 430 435 440	679
ACC GTG CAC CTC TCC TGT CAG GAG AAA CAG AAC ACC GTC TGC ACC TGC Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 445 450 455	727
CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC His Ala Gly Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn 460 465 470	775
TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TCC CTA CCC CAG ATT GAG Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Ser Leu Pro Gln Ile Glu 475 480 485	823
AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCC GGT GCT GCC CCA Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Ala Pro 490 495 500 505	871
GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro 510 515 520	919
GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr 525 530 535	967
CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val 540 545 550	1015
ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr 555 560 565	1063
GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser 570 575 580 585	1111
ACT TGT TAT TAT CAC AAA TCT TAAGGATCCCC TCGAG Thr Cys Tyr Tyr His Lys Ser 590	1147

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp  
1 5 10 15

Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile  
20 25 30

His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr  
35 40 45

Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg  
50 55 60

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His  
65 70 75 80

Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile  
85 90 95

Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn  
100 105 110

Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys  
115 120 125

Thr Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln  
130 135 140

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu  
145 150 155 160

Cys Val Ser Cys Ser Asn Cys Lys Ser Leu Glu Cys Thr Lys Leu  
165 170 175

Ser Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr  
180 185 190

Thr Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn  
195 200 205

Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys  
210 215 220

Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met  
225 230 235 240

Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys  
245 250 255

Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His  
260 265 270

Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser  
275 280 285

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 279..1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCGAGATGG	CTACAGGTAA	GCGCCCTAA	AATCCCTTG	GGCACAAATGT	GTCCTGAGGG	60
GAGAGGCAGC	GACCTGTAGA	TGGGACGGGG	GCACTAACCC	TCAGGTTTGG	GGCTTCTGAA	120
TGTGAGTATC	GCCATGTAAG	CCCAGTATT	GGCCAATGTC	AGAAAGCTCC	TGGCCCTGAA	180
AGGGATGGAG	AGAGAAAAAC	AAACACCTCC	TGGAGCAGGG	AGAGTGCTGC	CCTCTTGCTC	240
TCCGGCTCCC	TCTGTTGCC	TCTGGTTCT	CCCCAGGC	TCC CGG ACG	TCC CTG	293
			Ser Arg	Thr Ser	Leu	
			290			
CTC CTG GCT TTT	GGC CTG CTC	TGC CTG CCC	TGG CTT CAA	GAG GGC AGT		341
Leu Leu Ala	Phe Gly	Leu Leu Cys	Leu Pro	Trp Leu Gln	Glu Gly Ser	
295	300	305				
GCC GAT AGT GTG	TGT CCC CAA	GGA AAA TAT	ATC CAC CCT	CAA AAT AAT		389
Ala Asp Ser Val	Cys Pro Gln	Gly Lys Tyr	Ile His Pro	Gln Asn Asn		
310	315	320				
TCG ATT TGC TGT	ACC AAG TGC	CAC AAA GGA	ACC TAC TTG	TAC AAT GAC		437
Ser Ile Cys	Cys Thr Lys	Cys His Lys	Gly Thr Tyr	Leu Tyr Asn	Asp	
325	330	335				
TGT CCA GGC CCG	GGG CAG GAT	ACG GAC TGC	AGG GAG TGT	GAG AGC GGC		485
Cys Pro Gly	Pro Gly Gln	Asp Thr Asp	Cys Arg Glu	Cys Glu Ser	Gly	
340	345	350				
TCC TTC ACC GCT	TCA GAA AAC	CAC CTC AGA	CAC TGC CTC	AGC TGC TCC		533
Ser Phe Thr Ala	Ser Glu Asn	His Leu Arg	His Cys Leu	Ser Cys	Ser	
355	360	365	370			
AAA TGC CGA AAG	GAA ATG GGT	CAG GTG GAG	ATC TCT TCT	TGC ACA GTG		581
Lys Cys Arg	Lys Glu Met	Gly Gln Val	Glu Ile Ser	Ser Cys	Thr Val	
375	380	385				
GAC CGG GAC ACC	GTG TGT GGC	TGC AGG AAG	AAC CAG TAC	CGG CAT TAT		629
Asp Arg Asp	Thr Val Cys	Gly Cys Arg	Lys Asn Gln	Tyr Arg His	Tyr	
390	395	400				
TGG AGT GAA AAC	CTT TTC CAG	TGC TTC AAT	TGC AGC CTC	TGC CTC AAT		677
Trp Ser Glu Asn	Leu Phe Gln	Cys Phe Asn	Cys Ser	Leu Cys	Leu Asn	
405	410	415				
GGG ACC GTG CAC	CTC TCC TGC	CAG GAG AAA	CAG AAC ACC	GTG TGC ACC		725
Gly Thr Val His	Leu Ser Cys	Gln Glu Lys	Gln Asn Thr	Val Cys	Thr	
420	425	430				
TGC CAT GCA GGT	TTC TTT CTA	AGA GAA AAC	GAG TGT GTC	TCC TGT AGT		773
Cys His Ala	Gly Phe	Leu Arg Glu	Asn Glu	Cys Val Ser	Cys Ser	
435	440	445	450			

AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 455 460 465	821
GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCT GGT GCT GGT Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Gly 470 475 480	869
CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG AAG GAG GGC Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly 485 490 495	917
TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC GGC TAC TGC Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys 500 505 510	965
CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC CTG CCT CAG Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln 515 520 525 530	1013
GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC CGG CTC CCT Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro 535 540 545	1061
GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC GTG GCT CTC Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu 550 555 560	1109
AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC TGC GGG GGT Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly 565 570 575	1157
CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC CAG GAC TCC Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser 580 585 590	1205
TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA TCC CGA CTC Ser Ser Ser Lys Ala Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu 595 600 605 610	1253
CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA T AAGGATCCCT CGAG Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln 615 620	1301

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp 1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile 20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr 35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg 50 55 60

Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His
65										75				80	
Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile
	85							90						95	
Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn
	100							105						110	
Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys
	115								120					125	
Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln
	130							135					140		
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu
	145							150			155			160	
Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu
	165							170						175	
Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr
								180		185				190	
Thr	Ala	Gly	Ala	Gly	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala
	195							200						205	
Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile
	210							215			220				
Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val	Leu
	225							230			235			240	
Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe	Glu
									245		250			255	
Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val	Ser
								260		265			270		
Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser	Thr
								275		280			285		
Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp	Pro
	290							295			300				
Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu	Pro
	305							310			315			320	
Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln
								325		330			335		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Gly Ala Ala Pro Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Gly Ala Gly  
1

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTCTCGAG ATGGCTACAG GTAAGCGCCC

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCTGGGGCA GCACCGGCAC AGGAGACACA CTCGTTTC

39

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGCCGGTG CTGCCCCAGG TTGCCAGAA TGCACGCTAC AG

42

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTGGATCC TTAAGATTTG TGATAATAAC AAGTAC

36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTGGACCA GCACCAGCAC AGGAGACACA CTCGTTTC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTGCTGGTG CTGGTCCACG GTGCCGCCCG ATCAAT

36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTTGGATCC TTATTGTGGG AGGATCGGGG TG

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTTAGATCT CTTCTTGCAC AGTGGAC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGTGCCT GAGTCCTCAG T

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTGAGGACT CAGGCACCAC AGCCGGTGCT GCCCCAGGTT G

41

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTCTAGA GAAGCAGCAG CAGCCCAGT

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTCCACAG CCAGGGTGGC ATTGATGGGG CGGCACCGTG GACCAGCACC AGCTGTGGTG

60

CCTGAGTCCT CAGTG

75